

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.

(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE

(iii) NUMBER OF SEQUENCES: 41

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Abbott Laboratories
(B) STREET: 100 Abbott Park Road
(C) CITY: Abbott Park
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/850,713
(B) FILING DATE: 02-MAY-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Becker, Cheryl L.
(B) REGISTRATION NUMBER: 35,441
(C) REFERENCE/DOCKET NUMBER: 6083.US.P1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 847/935-1729
(B) TELEFAX: 847/938-2623
(C) TELEX:

109449-467-1850

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGGCTGTAC	CAGGGCGTGC	CCAGAGCTGA	GCCGGGCACC	GAGGCCCGGA	GACACTATGA	60
TGAAGGCGTT	CGGATGGGCA	GCCTGGGGCT	GTTCCTGCAG	TGCGCCATCT	CCCTGGTCTT	120
CTCTCTGGTC	ATGGACCGGC	TGGTGCAGCG	ATTCGGCACT	CGAGCAGTCT	ATTTGGCCAG	180
TGTGGCAGCT	TTCCCTGTGG	CTGCCGGTGC	CACATGCCTG	TCCCACAGTG	TGGCCGTGGT	240
GACAGCTTCA	GCCGCCTT					258

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACCAGGGCGT	GCCCAGAGCT	GAGCCGGGCA	CCGAGGCCCG	GAGACACTAT	GATGAAGGCG	60
TTCGGATGGG	CAGCCTGGGG	CTGTTCTGTC	AGTGCGCCAT	CTCCCTGGTC	TTCTCTCTGG	120
TCATGGACCG	GCTGGTGCAG	CGATTGGGCA	CTCGAGCAGT	CTATTTGGCC	AGTGTGGCAG	180
CTTTCCTGT	GGCTGCCGGT	GCCACATGCC	TGTCCCA			217

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 215
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GACAGCTTCA	GCCGCCCTCA	CCGGGTTTAC	CTTCTCAGCC	CTGCAGATCC	TGCCCTACAC	60
ACTGGCCTCC	CTCTACCACC	GGGAGAAGCA	GGTGTTCCTG	CCCAAATACC	GAGGGGACAC	120
TGGAGGTGCT	AGCAGTGAGG	ACAGCCTGAT	GACCAGCTTC	CTGCCAGGCC	CTAAGCCTGG	180
AGCTCCCTTC	CCTAATGGAC	ACGTGGGTGC	TGGANGCAGT	GGCCTGCTCC	CACCTCCACC	240
CGCGCTCTGC	GGGGC					255

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCTCCCTTCC	CTAATGGACA	CGTGGGTGCT	GGAGGCAGTG	GCCTGCTCCC	ACCTCCACCC	60
GCGCTCTGCG	GGGCCTCTGC	CTGTGATGTC	TCCGTACGTG	TGGTGGTGGG	TGAGCCCACC	120
GAGGCCAGGG	TGGTTCGGGG	CCGGGGCATC	TGCCTGGACC	TCGCCATCCT	GGATAGTGCC	180
TTCTTGCTGT	CCCAGGTGGC	CCCATCCCTG	TTTATGGGCT	CCATTGTCCA	GCTCAGCCAG	240
TCTGTCA						247

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGGATAGTGC	CTTCCTGCTG	TCCCAGGTGG	CCCCATCCCT	GTTTATGGGC	TCCATTGTCC	60
AGCTCAGCCA	GTCTGTCACT	GCCTATATGG	TGTCTGCCGC	AGGCTGGGTC	TGGTCGCCAT	120
TTACTTTGCT	ACACAGGTAG	TATTTGACAA	GAGCGACTTG	GCCAAATACT	CAGCGTAGAA	180
AACTTCCAGC	ACATTGGGGT	GGAGGGCCTG	CCTCACTGGG	TCCCAGCTCC	C	231

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 178
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTTGGCCAAA	TACTCAGCGT	AGAAAACCTC	CAGCACATTG	GGGTGGAGGG	CCTGCCTCAC	60
TGGGTCCCAG	CTCCCCGCTC	CTGTTAGCCC	CATGGGGCTG	CCGGGCTGGC	CGCCAGTTTC	120
TGTTGCTGCC	AAAGTAATGT	GGCTCTCTGC	TGCCACCCTG	TGCTGCTGAG	GTGCCGTANTG	180
CACAGCTGGG	GGCTG					195

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 67
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 222
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCCAGTTTCT	GTGCTGCCA	AAGTAATGTG	GCTCTCTGCT	GCCACCCTGT	GCTGCTGAGG	60
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TGCGTANTGC	ACAGCTGGGG	GCTGGGGCGT	CCCTCTCCTC	TCTCCCCAGT	CTCTAGGGCT	120
GCCTGACTGG	AGGCCTTCCA	AGGGGGTTTC	AGTCTGGACT	TATACAGGGA	GGCCAGAAGG	180
GCTCCATGCA	CTGGAATGCG	GGGACTCTGC	AGGTGGATTA	CNC		223

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 323
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCCAGAAGGG	CTCCATGCAC	TGGAATGCGG	GGACTCTGCA	GGTGGATTAC	CCAGGCTCAG	60
GGTTAACAGC	TAGCCTCCTA	GTTGAGACAC	ACCTAGAGAA	GGGTTTTTGG	GAGCTGAATA	120
AACTCAGTCA	CCTGGTTTCC	CATCTCTAAG	CCCCTTAACC	TGCAGCTTCG	TTTAATGTAG	180
CTCTTGCAIG	GGAGTTTCTA	GGATGAAACA	CTCCTCCATG	GGATTTGAAC	ATATGAAAGT	240
TATTTGTAGG	GGAAGAGTCC	TGAGGGGCAA	CACACAAGAA	CCAGGTCCCC	TCAGCCCACA	300
GCACTGTCTT	TTTGCTGATC	CANCCCCCTC	TTACTTTTAT	CA		342

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGAAGAGT	CCTGAGGGGC	AACACACAAG	AACCAGGTCC	CCTCAGCCCA	CAGCACTGTC	60
TTTTTGCTGA	TCCACCCCCC	TCTTACCTTT	TATCAGGATG	TGGCCTGTTG	GTCCTTCTGT	120
TGCCATCACA	GAGACACAGG	CATTAAATA	TTTAACTTAT	TTATTTAACA	AAGTAGAAGG	180
GAATCCATTG	CTAGCTTTTC	TGTGTTGGTG	TCTAATATTT	GGGTAGGGTG	GGGGATCCCC	240
AACAATCAGG	TCCCCTGAGA	TAGCT				265

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 147
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTCTTACCTT	TTATCAGGAT	GTGGCCTGTT	GGTCCTTCTG	TTGCCATCAC	AGAGACACAG	60
GCATTTAAAT	ATTTAACTTA	TTTATTTAAC	AAAGTAGAAG	GGAATCCATT	GCTAGCTTTT	120
CTGTGTTGGT	GTCTAATATT	TGGGTANGGT	GGGGGATCCC	CAACAATCAG	GTCCCCCTGAG	180
ATAGCTGGTC	ATTGGGCTGA	TCATTGCCAG	AATCTTCTTC	TCCTGGGGTC	TGGCCCCCCA	240
AAATGCCTAA	CCCAGGACCT	TGGAAATTCT	ACTCATCCCA	AATGATAA		288

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 216
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAATTCTACT	CATCCCAAAT	GATAATTCCA	AATGCTGTTA	CCCAAGGTTA	GGGTGTTGAA	60
GGAAGGTAGA	GGGTGGGGCT	TCAGGTCTCA	ACGGCTTCCC	TAACCACCCC	TCTTCTCTTG	120
GCCCAGCCTG	GTTCCCCCA	CTTCCACTCC	CCTCTACTCT	CTCTAGGACT	GGGCTGATGA	180
AGGCACTGCC	CAAATTTCC	CCTACCCCA	ACTTTNCCCT	ACCCCAACT	TTCCCCACCA	240
GCTCCACAAC	CCTGTTTGA	GCTACTGCAG	GT			272

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 197
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AAGGCACTGC	CCAAAATNNC	CCCTACCCCC	AACTTTCCCC	TACCCCAAC	TTTCCCCACC	60
AGCTCCACAA	CCCTGTTTGG	AGCTACTGCA	GGACCAGAAG	CACAAAGTGC	GGTTTCCCAA	120
GCCTTTGTCC	ATCTCAGCCC	CCAGAGTATA	TCTGTGCTTG	GGGAATCTCA	CACAGAAACT	180
CAGGAGCACC	CCCTGCNTGA	GCTAAGGGAG	GTCTTATCTC	TCAGGGGGGG	TTTAAGTGCC	240
GTTTGCAATA	ATGTCGTCTT	ATTTATTTAG	CGGGGTGAAT	ATTTTATACT	GTAA	294

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 113
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 147
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCCACAACC	CTGTTTGGAG	CTACTGCAGG	ACCAGAAGCA	CAAAGTGCGG	TTTCCCAAGC	60
CTTTGTCCAT	CTCAGCCCCC	AGAGTATATC	TGTGCTTGGG	GAATCTCACA	CANAAACTCA	120
GGAGCACCCC	CTGCCTGAGC	TAAGGGNGGT	C			151

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCCAGAGTAT	ATCTGTGCTT	GGGGAATCTC	ACACAGAAAC	TCAGGAGCAC	CCCCTGCCTG	60
AGCTAAGGGA	GGTCTTATCT	CTCAGGGGGG	GTTTAAGTGC	CGTTTGCAAT	AATGTCGTCT	120
TATTTATTTA	GCGGGGTGAA	TATTTTATAC	TGTAAGTGAG	CAATCAGAGT	ATAATGTTTA	180
TGGTGACAAA	ATTAAAGGCT	TTCTTATATG	TTT			213

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACCAGGGCGT	GCCCAGAGCT	GAGCCGGGCA	CCGAGGCCCCG	GAGACACTAT	GATGAAGGCG	60
TTCGGATGGG	CAGCCTGGGG	CTGTTCTCTG	AGTGCGCCAT	CTCCCTGGTC	TTCTCTCTGG	120
TCATGGACCG	GCTGGTGAG	CGATTGCGCA	CTCGAGCAGT	CTATTTGGCC	AGTGTGGCAG	180
CTTTCCCTGT	GGCTGCCGGT	GCCACATGCC	TGTCCCACAG	TGTGGCCGTG	GTGACAGCTT	240
CAGCCGCCCT	CACCGGGTTC	ACCTTCTCAG	CCCTGCAGAT	CCTGCCCTAC	ACACTGGCCT	300
CCCTCTACCA	CCGGGAGAAG	CAGGTGTTCC	TGCCCCAATA	CCGAGGGGAC	ACTGGAGGTG	360
CTAGCAGTGA	GGACAGCCTG	ATGACCAGCT	TCCTGCCAGG	CCCTAAGCCT	GGAGCTCCCT	420
TCCCTAATGG	ACACGTGGGT	GCTGGAGGCA	GTGGCCTGCT	CCCACCTCCA	CCCGCGCTCT	480
GCGGGGCCTC	TGCCTGTGAT	GTCTCCGTAC	GTGTGGTGGT	GGGTGAGCCC	ACCGAGGCCA	540
GGGTGGTTCC	GGGCCGGGGC	ATCTGCCTGG	ACCTCGCCAT	CCTGGATAGT	GCCTTCCTGC	600
TGTCCCAGGT	GGCCCCATCC	CTGTTTATGG	GCTCCATTGT	CCAGCTCAGC	CAGTCTGTCA	660
CTGCCTATAT	GGTGTCTGCC	GCAGGCCTGG	GTCTGGTCGC	CATTTACTTT	GCTACACAGG	720
TAGTATTTGA	CAAGAGCGAC	TTGGCCAAAT	ACTCAGCGTA	GAAAACCTTC	AGCACATTGG	780
GGTGGAGGGC	CTGCCTCACT	GGGTCCCAGC	TCCCCGCTCC	TGTTAGCCCC	ATGGGGCTGC	840
CGGGCTGGCC	GCCAGTTTCT	GTTGCTGCCA	AAGTAATGTG	GCTCTCTGCT	GCCACCCTGT	900
GCTGCTGAGG	TGCGTAGCTG	CACAGCTGGG	GGCTGGGGCG	TCCCTCTCCT	CTCTCCCCAG	960
TCTCTAGGGC	TGCCTGACTG	GAGGCCTTCC	AAGGGGGTTT	CAGTCTGGAC	TTATACAGGG	1020
AGGCCAGAAG	GGCTCCATGC	ACTGGAATGC	GGGACTCTGC	AGGTGGATTA	CCCAGGCTCA	1080
GGGTTAACAG	CTAGCCTCCT	AGTTGAGACA	CACCTAGAGA	AGGGTTTTTG	GGAGCTGAAT	1140
AAACTCAGTC	ACCTGGTTTC	CCATCTCTAA	GCCCCCTAAC	CTGCAGCTTC	GTTTAATGTA	1200
GCTCTTGCA	T	AGGATGAAAC	ACTCCTCCAT	GGGATTTGAA	CATATGAAAG	1260
TTATTTGTAG	GGAAGAGTC	CTGAGGGGCA	ACACACAAGA	ACCAGGTCCC	CTCAGCCCAC	1320

AGCACTGTCT	TTTTGCTGAT	CCACCCCCCT	CTTACCTTTT	ATCAGGATGT	GGCCTGTTGG	1380
TCCTTCTGTT	GCCATCACAG	AGACACAGGC	ATTTAAATAT	TTAACTTATT	TATTTAACAA	1440
AGTAGAAGGG	AATCCATTGC	TAGCTTTTCT	GTGTTGGTGT	CTAATATTTG	GGTAGGGTGG	1500
GGGATCCCCA	ACAATCAGGT	CCCCTGAGAT	AGCTGGTCAT	TGGGCTGATC	ATTGCCAGAA	1560
TCTTCTTCTC	CTGGGGTCTG	GCCCCCAAA	ATGCCTAACC	CAGGACCTTG	GAAATTCTAC	1620
TCATCCCAAA	TGATAATTCC	AAATGCTGTT	ACCCAAGGTT	AGGGTGTTGA	AGGAAGGTAG	1680
AGGGTGGGGC	TTCAGGTCTC	AACGGCTTCC	CTAACCACCC	CTCTTCTCTT	GGCCCAGCCT	1740
GGTTCCCCCC	ACTTCCACTC	CCCTCTACTC	TCTCTAGGAC	TGGGCTGATG	AAGGCACTGC	1800
CCAAAATTTT	CCCTACCCCC	AACTTTCCCC	TACCCCCAAC	TTTCCCCACC	AGCTCCACAA	1860
CCCTGTTTGG	AGCTACTGCA	GGACCAGAAG	CACAAAGTGC	GGTTTCCCAA	GCCTTTGTCC	1920
ATCTCAGCCC	CCAGAGTATA	TCTGTGCTTG	GGGAATCTCA	CACAGAAACT	CAGGAGCACC	1980
CCCTGCCTGA	GCTAAGGGAG	GTCTTATCTC	TCAGGGGGGG	TTTAAGTGCC	GTTTGCAATA	2040
ATGTCGTCTT	ATTTTTTTAG	CGGGGTGAAT	ATTTTATACT	GTAAGTGAGC	AATCAGAGTA	2100
TAATGTTTAT	GGTGACAAAA	TTAAAGGCTT	TCTTATATGT	TTA		2143

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGGGCTGTAC	CAGGGCGTGC	CCAGAGCTGA	GCCGGGCACC	GAGGCCCGGA	GACACTATGA	60
TGAAGGCGTT	CGGATGGGCA	GCCTGGGGCT	GTTCCCTGCAG	TGCGCCATCT	CCCTGGTCTT	120
CTCTCTGGTC	ATGGACCGGC	TGGTGCAGCG	ATTCGGCACT	CGAGCAGTCT	ATTTGGCCAG	180
TGTGGCAGCT	TTCCCTGTGG	CTGCCGGTGC	CACATGCCTG	TCCCACAGTG	TGGCCGTGGT	240
GACAGCTTCA	GCCGCCCTCA	CCGGGTTCAC	CTTCTCAGCC	CTGCAGATCC	TGCCCTACAC	300
ACTGGCCTCC	CTCTACCACC	GGGAGAAGCA	GGTGTTCCCTG	CCCAAATACC	GAGGGGACAC	360
TGGAGGTGCT	AGCAGTGAGG	ACAGCCTGAT	GACCAGCTTC	CTGCCAGGCC	CTAAGCCTGG	420
AGCTCCCTTC	CCTAATGGAC	ACGTGGGTGC	TGGAGGCAGT	GGCCTGCTCC	CACCTCCACC	480
CGCGCTCTGC	GGGGCCTCTG	CCTGTGATGT	CTCCGTACGT	GTGGTGGTGG	GTGAGCCCAC	540
CGAGGCCAGG	GTGGTTCCGG	GCCGGGGCAT	CTGCCTGGAC	CTCGCCATCC	TGGATAGTGC	600
CTTCTGTCTG	TCCCAGGTGG	CCCCATCCCT	GTTTATGGGC	TCCATTGTCC	AGCTCAGCCA	660
GTCTGTCACT	GCCTATATGG	TGTCTGCCGC	AGGCCTGGGT	CTGGTCGCCA	TTTACTTTGC	720
TACACAGGTA	GTATTTGACA	AGAGCGACTT	GGCCAAATAC	TCAGCGTAGA	AAACTTCCAG	780
CACATTGGGG	TGGAGGGCCT	GCCTCACTGG	GTCCCAGCTC	CCCGCTCCTG	TTAGCCCCAT	840
GGGGCTGCCG	GGCTGGCCGC	CAGTTTCTGT	TGCTGCCAAA	GTAATGTGGC	TCTCTGCTGC	900
CACCCTGTGC	TGCTGAGGTG	CGTAGCTGCA	CAGCTGGGGG	CTGGGGCGTC	CCTCTCCTCT	960
CTCCCCAGTC	TCTAGGGCTG	CCTGACTGGA	GGCCTTCCAA	GGGGGTTTCA	GTCTGGACTT	1020
ATACAGGGAG	GCCAGAAGGG	CTCCATGCAC	TGGAATGCGG	GGACTCTGCA	GGTGGATTAC	1080
CCAGGCTCAG	GGTTAACAGC	TAGCCTCCTA	GTTGAGACAC	ACCTAGAGAA	GGGTTTTTGG	1140
GAGCTGAATA	AACTCAGTCA	CCTGGTTTCC	CATCTCTAAG	CCCCTTAACC	TGCAGCTTCG	1200
TTTAATGTAG	CTCTTGCAATG	GGAGTTTCTA	GGATGAAACA	CTCCTCCATG	GGATTTGAAC	1260
ATATGAAAGT	TATTTGTAGG	GGAAGAGTCC	TGAGGGGGCA	CACACAAGAA	CCAGGTCCCC	1320
TCAGCCCACA	GCACTGTCTT	TTTGCTGATC	CACCCCCCTC	TTACCTTTTA	TCAGGATGTG	1380
GCCTGTTGGT	CCTTCTGTTG	CCATCACAGA	GACACAGGCA	TTTAAATATT	TAACCTATTT	1440
ATTTAACAAA	GTAGAAGGGA	ATCCATTGCT	AGCTTTTCTG	TGTTGGTGTG	TAATATTTGG	1500
GTAGGGTGGG	GGATCCCCAA	CAATCAGGTC	CCCTGAGATA	GCTGGTCAAT	GGGCTGATCA	1560
TTGCCAGAAT	CTTCTTCTCC	TGGGGTCTGG	CCCCCAAAA	TGCCTAACCC	AGGACCTTGG	1620
AAATTCTACT	CATCCCAAAT	GATAATTCCA	AATGCTGTTA	CCCAAGGTTA	GGGTGTTGAA	1680
GGAAGGTAGA	GGGTGGGGCT	TCAGGTCTCA	ACGGCTTCCC	TAACCACCCC	TCTTCTCTTG	1740
GCCCAGCCTG	GTTCCCCCCA	CTTCCACTCC	CCTCTACTCT	CTCTAGGACT	GGGCTGATGA	1800
AGGCACTGCC	CAAAATTTCC	CCTACCCCCA	ACTTTCCCCT	ACCCCCAACT	TTCCCCACCA	1860
GCTCCACAAC	CCTGTTTGGG	GCTACTGCAG	GACCAGAAGC	ACAAAGTGCG	GTTTCCCAAG	1920
CCTTTGTCCA	TCTCAGCCCC	CAGAGTATAT	CTGTGCTTGG	GGAATCTCAC	ACAGAAACTC	1980
AGGAGCACCC	CCTGCCTGAG	CTAAGGGAGG	TCTTATCTCT	CAGGGGGGGT	TTAAGTGCCG	2040
TTTGCAATAA	TGTCGTCTTA	TTTATTTAGC	GGGGTGAATA	TTTTATACTG	TAAGTGAGCA	2100
ATCAGAGTAT	AATGTTTATG	GTGACAAAAT	TAAAGGCTTT	CTTATATGTT	TA	2152

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC 60
CGGGAATT 68

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG 60
GAATTCCG 68

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCGGATAAC AATTTACAC AGGA 24

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGTAAAACGA CGGCCAGT 18

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGTTCTGCC CAAATACC 18

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGTCTGGTCG CCATTAC

18

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGGGCAACAC ACAAGAAC

18

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCAGCCCCCA GAGTATATC

19

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCTCCATGCA CTGGAATG

18

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ACCCAGGACC TTGGAAAT

18

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

105240-464460

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ACACCCTAAC CTTGGGTAAC

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCTAGAAACT CCCATGCAAG

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TGGCAGCAAC AGAAACTG

18

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ACTATCCAGG ATGGCGAG

18

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGATTGCTCA CTTACAGT

18

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGGTTAGGGA AGCCGTTG

18

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGCCCAATGA CCAGCTAT

18

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTCCAAATGC TGTTACCCAA GG

22

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGTGCTCCTG AGTTTCTGTG TGAG

24

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro	Gly	Thr	Glu	Ala	Arg	
1				5					10					15		
Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	Ser	Leu	Gly	Leu	Phe	Leu	
			20					25					30			
Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	Val	Met	Asp	Arg	Leu	Val	
	35						40					45				

Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr	Leu	Ala	Ser	Val	Ala	Ala	Phe
50						55					60				
Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu	Ser	His	Ser	Val	Ala	Val	Val
65					70					75					80
Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe	Thr	Phe	Ser	Ala	Leu	Gln	Ile
				85					90					95	
Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	Arg	Glu	Lys	Gln	Val	Phe
			100					105					110		
Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	Ala	Ser	Ser	Glu	Asp	Ser
		115				120						125			
Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro	Lys	Pro	Gly	Ala	Pro	Phe	Pro
	130					135					140				
Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu	Leu	Pro	Pro	Pro	Pro
145					150					155					160
Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp	Val	Ser	Val	Arg	Val	Val	Val
				165					170					175	
Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	Gly	Arg	Gly	Ile	Cys	Leu
			180					185					190		
Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	Leu	Ser	Gln	Val	Ala	Pro
	195					200						205			
Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	Ser	Gln	Ser	Val	Thr	Ala
	210					215					220				
Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	Val	Ala	Ile	Tyr	Phe	Ala
225					230					235					240
Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp	Leu	Ala	Lys	Tyr	Ser	Ala	
				245					250					255	

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Tyr	His	Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr
1				5					10					15	
Gly	Gly	Ala	Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly
			20					25					30		
Pro	Lys	Pro	Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val				
		35					40								

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	Gly	Arg
1				5					10					15	
Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser					
			20					25							

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro	Gly	Thr	Glu	Ala	Arg
1				5					10					15	
Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	Ser					
			20					25							

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys
1				5			

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Met	His	Thr	Glu	His
1				5					10					15	
His	His	His	His	His											
				20											

105410-1054150